

SEQUENCE LISTING

<110> Allen, Steve
Zhu, Qun

<120> PLANT GENES ENCODING DR1 AND DRAP1, A GLOBAL REPRESSOR COMPLEX OF
TRANSCRIPTION

<130> BB1107 US CIP

<140> US/09/789,054

<141> 2001-02-20

<150> 09/485558

<151> 2000-02-11

<150> PCT/US98/16688

<151> 1998-08-12

<150> 60/055,865

<151> 1997-08-15

<160> 69

<170> Microsoft Office 97

<210> 1

<211> 400

<212> DNA

<213> Zea mays

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<212> PRT

<213> Zea mays

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Ser Val Pro Cys Val Glu Met Asp Pro Met Asp Ile Val Gly Lys Ser
      35              40              45

Lys Glu Asp Val Ser Leu Pro Lys Ser Thr Met Val Lys Ile Ile Lys
      50              55              60

Glu Met Leu Pro Pro Asp Val Arg Val Ala Arg Asp Ala Gln Asp Leu
      65              70              75              80
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Leu Val Glu Cys Cys Val Glu Phe Ile Asn Leu Leu Ser Ser Glu Ser
85 90 95

Asn Glu Val Cys Ser Arg Glu Glu Lys Lys Thr Ile Ala Pro Glu His
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Val Ile Lys Ala Leu Ser Asp Leu Gly Phe Arg Glu Tyr Ile Glu Glu
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Val Tyr Ala Ala
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<213> Zea mays

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Val Pro Cys Val Glu Met Asp Pro Met Asp Ile Val Gly Lys Ser Lys
35 40 45

Glu Asp Val Ser Leu Pro Lys Ser Thr Met Val Lys Ile Ile Lys Glu
 50 55 60
 Met Leu Pro Pro Asp Val Arg Val Ala Arg Asp Ala Gln Asp Leu Leu
 65 70 75 80
 Val Glu Cys Cys Val Glu Phe Ile Asn Leu Leu Ser Ser Glu Ser Asn
 85 90 95
 Glu Val Cys Ser Arg Glu Glu Lys Lys Thr Ile Ala Pro Glu His Val
 100 105 110
 Ile Lys Ala Leu Ser Asp Leu Gly Phe Arg Glu Tyr Ile Glu Glu Val
 115 120 125
 Tyr Ala Ala Tyr Glu Gln His Lys Leu Glu Thr Leu Asp Ser Pro Lys
 130 135 140
 Ala Gly Lys Phe Thr Arg Ile Glu Met Thr Glu Glu Glu Ala Val Ala
 145 150 155 160
 Glu Gln Gln Arg Met Phe Ala Glu Ala Arg Ala Arg Met Asn Asn Gly
 165 170 175
 Ala Pro Lys Pro Lys Glu Pro Glu Gln Glu Pro Pro Gln Leu Pro Gln
 180 185 190
 Ala Gln Pro Gln Leu Gln Leu His Thr Glu Pro Gln Gln Pro Met Gln
 195 200 205
 Ser Gln Val Gln Leu His Ser Gln Thr Gln His Tyr Leu Gln Pro Gln
 210 215 220
 Leu Gln Leu His His Gln Pro Gln Gln Leu Pro Gln Val Gln Leu His
 225 230 235 240
 Ser Gln Pro Gln Leu Gln Pro Gln Val His Leu His Pro Gln Pro Gln
 245 250 255
 Leu Pro Pro Gln Leu Gln Val His Gln Gln Leu Gln Gln Pro Pro Gln
 260 265 270
 Val Gln Val His Gln Gln Pro Glu Val Gln Pro Gln Glu Ala Gln Leu
 275 280 285
 Gln Ser Ser Ala Gln Gln Thr Ser Gln Pro Gln Pro Gln Ala Gln Leu
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 <211> 1316
 <212> DNA
 <213> Zea mays

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tgtttaagat aattaaggag atgcttcctc ctgatgtacg agtggcaaga gatgcacagg 240
atcttcttgt tgaatgctgt gtagagttca tcaatctcct ttcgtctgaa tcgaatgaag 300
tgtgcagcag agaagagaaa aaaacgattg ctccctgagca tgttatcaag gctctaagtg 360
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<210> 6
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<212> PRT
<213> Zea mays

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      20             25             30

Asp Ser Leu Leu Arg Leu Glu Met Asp Pro Met Asp Ile Val Gly Lys
      35             40             45

Ser Lys Glu Asp Val Ser Leu Pro Lys Ser Thr Met Phe Lys Ile Ile
      50             55             60

Lys Glu Met Leu Pro Pro Asp Val Arg Val Ala Arg Asp Ala Gln Asp
      65             70             75             80

Leu Leu Val Glu Cys Cys Val Glu Phe Ile Asn Leu Leu Ser Ser Glu
      85             90             95

Ser Asn Glu Val Cys Ser Arg Glu Glu Lys Lys Thr Ile Ala Pro Glu
      100            105            110

His Val Ile Lys Ala Leu Ser Asp Leu Gly Phe Arg Glu Tyr Ile Glu
      115            120            125

Glu Val Tyr Ala Ala Tyr Glu Gln His Lys Leu Asp Thr Leu Asp Ser
      130            135            140

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Pro Lys Ala Gly Lys Phe Thr Gly Ile Glu Met Thr Glu Glu Glu Ala
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 165 170 175
 Asn Gly Ala Pro Lys Pro Lys Glu Thr Glu Gln Glu Pro Pro Gln Gln
 180 185 190
 Pro Gln Ala Gln Pro Gln Leu Gln Leu His Thr Glu Pro Gln Gln Pro
 195 200 205
 Val Gln Ser Gln Val Gln Leu His Ser Pro Thr Gln His Ser Leu Gln
 210 215 220
 Pro Gln Val Gln Leu His Pro Gln Pro Gln Gln Leu Pro Gln Val Gln
 225 230 235 240
 Val His Ser Gln Thr Gln Leu His Pro Gln Pro Gln Gln Pro Gln Val
 245 250 255
 Gln Val His Pro Gln Leu Gln Gln Leu Pro Gln Leu Gln Ala His Ser
 260 265 270
 Gln Pro Pro Gln Pro Gln Val Gln Ile His Pro Gln Pro Gln Gln Pro
 275 280 285
 Pro Gln Val Gln Leu Gln Ser Ser Val Gln Gln Thr Ser Gln Pro Gln
 290 295 300
 Pro Gln Val His Leu Tyr Asn His Arg Gly Gly Ser Gln Ala Gln Leu
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 <212> DNA
 <213> Oryza sp.

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 <222> (178)
 <223> n=a,c,g or t

<220>
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 <222> (196)
 <223> n=a,c,g or t

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 tgtagtacat cgtcancatc atttc 205

<210> 8
 <211> 38
 <212> PRT
 <213> Oryza sp.

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 Leu Ser Phe Pro Glu Tyr
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<210> 9
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 <212> DNA
 <213> Oryza sativa

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<210> 10
 <211> 296
 <212> PRT
 <213> Oryza sativa

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Val Arg Val Ala Arg Asp Ala Gln Asp Leu Leu Val Glu Cys Cys Val
 35 40 45
 Glu Phe Ile Asn Leu Leu Ser Ser Glu Ser Asn Glu Val Cys Ser Arg
 50 55 60
 Glu Asp Lys Lys Thr Ile Ala Pro Glu His Val Leu Arg Ala Leu Gln
 65 70 75 80
 Asp Leu Gly Phe Arg Glu Tyr Ile Glu Glu Val Gln Ala Ala Tyr Glu
 85 90 95
 His His Lys His Asp Thr Leu Asp Ser Pro Lys Ala Ser Lys Phe Thr
 100 105 110
 Gly Val Glu Met Thr Glu Glu Gln Ala Val Ala Glu Gln Gln Arg Met
 115 120 125
 Phe Ala Glu Ala Arg Ala Arg Met Asn Asn Gly Ala Ala Lys Pro Lys
 130 135 140
 Glu Pro Glu Pro Glu Ala Gln Gln Gln Thr Gln Gln Pro Pro Gln Pro
 145 150 155 160
 Gln Leu His Pro Gln Pro Gln Gln Pro Leu Gln Pro Gln Leu Gln Leu
 165 170 175
 His Pro Gln Pro Gln Gln Gln Pro Ser Gln Leu His Pro Gln Gln Leu
 180 185 190
 Leu His Pro Gln Ser Gln Gln Thr Pro Gln Pro Gln Pro Gln Val His
 195 200 205
 Pro Gln Pro Gln Gln Pro Pro Gln Leu Gln Pro Gln Pro Gln Leu Leu
 210 215 220
 Gln Gln Pro Gln Leu Pro Gln Gln Leu Gln Pro Gln Ser Gln Leu Pro
 225 230 235 240
 Pro Gln Pro Gln Gln Pro Pro Gln Leu Gln Leu Gln Ser Gln Leu His
 245 250 255
 Pro Gln Pro Gln Gln Pro Pro Gln Leu Gln Pro Gln Pro Gln Leu His
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<222> (433)

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<220>

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<223> n=a,c,g or t

<220>

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<223> n=a,c,g or t

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<222> (547)

<223> n=a,c,g or t

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<210> 12

<211> 98
 <212> PRT
 <213> Glycine max

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 <223> Xaa=ANY AMINO ACID

<220>
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 <222> (92)
 <223> Xaa=ANY AMINO ACID

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 35 40 45
 Glu Phe Ile Asn Leu Val Ser Ser Glu Xaa Asn Glu Val Cys Asn Lys
 50 55 60
 Glu Glu Arg Arg Thr Ile Ala Pro Glu His Val Leu Lys Ala Leu Gly
 65 70 75 80
 Val Leu Gly Phe Gly Glu Tyr Ile Glu Glu Val Xaa Ala Ala Tyr Glu
 85 90 95

Gln His

<210> 13
 <211> 885
 <212> DNA
 <213> Glycine max

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<211> 192
 <212> PRT
 <213> Glycine max

<400> 14

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			20					25					30		
Leu	Phe	Phe	Arg	Met	Glu	Pro	Met	Asp	Ile	Val	Gly	Lys	Ala	Lys	Glu
		35					40					45			
Asp	Ala	Ser	Leu	Pro	Lys	Ala	Thr	Met	Thr	Lys	Ile	Ile	Lys	Glu	Met
	50					55					60				
Leu	Pro	Pro	Asp	Val	Arg	Val	Ala	Arg	Asp	Ala	Gln	Asp	Leu	Leu	Ile
65					70					75					80
Glu	Cys	Cys	Val	Glu	Phe	Ile	Asn	Leu	Val	Ser	Ser	Glu	Ser	Asn	Glu
				85					90					95	
Val	Cys	Asn	Lys	Glu	Glu	Arg	Arg	Thr	Ile	Ala	Pro	Glu	His	Val	Leu
			100					105					110		
Lys	Ala	Leu	Gly	Val	Leu	Gly	Phe	Gly	Glu	Tyr	Ile	Glu	Glu	Val	Tyr
		115					120					125			
Ala	Ala	Tyr	Glu	Gln	His	Lys	Leu	Glu	Thr	Met	Gln	Asp	Ser	Leu	Lys
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Gly	Ala	Lys	Trp	Ser	Asn	Arg	Ala	Glu	Met	Thr	Glu	Glu	Glu	Ala	Leu
145					150					155					160
Ala	Glu	Gln	Gln	Arg	Met	Phe	Ala	Glu	Ala	Arg	Ala	Arg	Met	Asn	Gly
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Gly	Ala	Ile	Gln	Ser	Lys	Glu	Pro	Glu	Ala	Asp	Gln	Ser	Leu	Glu	Ser
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<400> 15

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gtttagatag	ctaactttag	gatctttatt	gaagcatagg	caagcaccac	cctgactcct	540
cctgtctgtg	ctttcaatta	gctcgattgt	gtacaaaaac	cgttcactag	tctgccggcc	600
tatgtggatg	tgctcatttg	tattctatcg	atgaatccat	atttgtaagt	caatgtaatt	660
agtgagagat	catgaaaacc	ctttcgttta	gcatttactt	gtaattattt	aatttacttt	720

ttgtatcttc tacatactaa caactcctag cttgattctg acagtagcta tatgttagat 780
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 aaa 843

<210> 16
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 <212> PRT
 <213> Glycine max

<400> 16
 Met Glu Pro Met Asp Ile Val Gly Lys Ser Lys Glu Asp Ala Ser Leu
 1 5 10 15
 Pro Lys Ala Thr Met Thr Lys Ile Ile Lys Glu Met Leu Pro Pro Asp
 20 25 30
 Phe Ile Asn Leu Val Ser Ser Glu Ser Asn Glu Val Cys Asn Arg Glu
 35 40 45
 Asp Lys Arg Thr Ile Ala Pro Glu His Val Leu Lys Ala Leu Gln Val
 50 55 60
 Leu Gly Phe Cys Glu Tyr Ile Glu Glu Val Tyr Ala Ala Tyr Glu Gln
 65 70 75 80
 His Lys Leu Glu Thr Met Gln Asp Ser Leu Arg Gly Gly Gly Gly Gly
 85 90 95
 Gly Lys Trp Asn Asn Gly Ala Glu Met Thr Glu Glu Glu Ala Leu Ala
 100 105 110
 Glu Gln Gln Arg Met Leu Ala Glu Ala Arg Ala Arg Met Asn Gly Gly
 115 120 125
 Ala Ile Ala Ser Lys Gln Pro Asp Ala Asp Gln Ser Leu Asp Ser
 130 135 140

<210> 17
 <211> 509
 <212> DNA
 <213> Triticum sp.

<220>
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 <222> (396)
 <223> n=a,c,g or t

<220>
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 <222> (415)
 <223> n=a,c,g or t

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 <222> (464)
 <223> n=a,c,g or t

<220>
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<222> (495)
 <223> n=a,c,g or t

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 cggcgccccc aggtcaagc tccgtcgcgc tttcgacggc gagggatgga tccgatggac 180
 atcgtgggca agtccaagga ggacgtctcc ctccccaaat caacaatgac caagattatt 240
 aaggagatgc taccgcctga tggtcgagta gcaagagata cacaggatct tcttggtgaa 300
 tgctgtgtag agttcatcaa tcttctttct tcgggaatcc aatgacgtgt gcagccggga 360
 cgacaagaaa actattgccc ctgaacatgt tattanggct ttgcaggatc ttggnttcaa 420
 ggagtatgtt gaagaagttt atgcagccta cgaacaacac aagnttgaaa cctggactct 480
 caaaagcaac caaantcact ggcatagaa 509

<210> 18
 <211> 113
 <212> PRT
 <213> Triticum sp.

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 <221> UNSURE
 <222> (57)
 <223> Xaa=ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (77)
 <223> Xaa=ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (100)
 <223> Xaa=ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (110)
 <223> Xaa=ANY AMINO ACID

<400> 18
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 1 5 10 15
 Pro Lys Ser Thr Met Thr Lys Ile Ile Lys Glu Met Leu Pro Pro Asp
 20 25 30
 Val Arg Val Ala Arg Asp Thr Gln Asp Leu Leu Val Glu Cys Cys Val
 35 40 45
 Glu Phe Ile Asn Leu Leu Ser Ser Xaa Ser Asn Asp Val Cys Ser Arg
 50 55 60
 Asp Asp Lys Lys Thr Ile Ala Pro Glu His Val Ile Xaa Ala Leu Gln
 65 70 75 80
 Asp Leu Gly Phe Lys Glu Tyr Val Glu Glu Val Tyr Ala Ala Tyr Glu
 85 90 95
 Gln His Lys Xaa Glu Thr Trp Thr Leu Lys Ser Asn Gln Xaa His Trp
 100 105 110

His

<210> 19

<211> 1463

<212> DNA

<213> Triticum aestivum

<400> 19

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ccggcgccgg cgcccccagg ctcaagctcc gtcgcgcttt cgacggcgag ggatggatcc 180
gatggacatc gtgggcaagt ccaaggagga cgtctccctc cccaaatcaa caatgaccaa 240
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tgttgaatgc tgtgtagagt tcatcaatct tctttcttcg gaatccaatg acgtgtgcag 360
ccgggacgac aagaaaacta ttgccctga acatgttatt agggctttgc aggatcttgg 420
cttcaaggag tatgttgaag aagtttatgc agcctacgaa cagcacaagc ttgaaaccct 480
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tgaacagcag agaatgtttg ctgaagcccg agcaaggatg aacaatggag ctgccaaacc 600
aaaggagcct gcattagaac cacagaatca accccaacag cccccacaac ctcatctgca 660
gctgcatcct caagcacagc agcctccaca acctcaaccg caactgcatc atcctcaatc 720
acagcagccc ctgcatcctc aactgcaacc gtatactcag gctccaccac agcagcccct 780
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gcagctgtat cctcaggctc aacctgagca acccctgcag cctcaatcct caggatcaac 900
cacaggaacc tgtgtaatct caactgccgc tccatctgca accggcacca ctgctgctgc 960
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tgcaagtgcc gctgccggcg ctgccgcaac ctcaaccca gccacctgaa ctgcagcagc 1080
cccagccgct aacacaactg caagcggaac atggcctgaa ctggacagtt agtggttcgg 1140
aacatgtagc gtcactataa gttaagactc tgcctccttt aaaattgtgc gttaggtttg 1200
cctgcatctt gtacaatgta aatcgtgtgt gatttcagcc accgtgtctc taataatctg 1260
aagctctcta gtaagcgatg tacttactgc gctggatact gtgtttatga ctggtttagt 1320
ctcatggtat tgtgtgtgac gtgtcagaag ctactccatt accagtgtaa tcaattgcct 1380
gacttaatgt tcacccgtga tgatagtaat tgatttcagt gtgctaataa aaaaaaaaaa 1440
aaaaaaaaaa aaaaaaaaaa aaa 1463
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<210> 20

<211> 348

<212> PRT

<213> Triticum aestivum

<400> 20

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Pro Ser Pro Pro Ser Pro Ser Ser Gly Pro Pro Val Pro Gly Gly Thr
      20                      25                      30

Arg Arg Arg Arg Arg Pro Gln Ala Gln Ala Pro Ser Arg Phe Arg Arg
      35                      40                      45

Arg Gly Met Asp Pro Met Asp Ile Val Gly Lys Ser Lys Glu Asp Val
      50                      55                      60

Ser Leu Pro Lys Ser Thr Met Thr Lys Ile Ile Lys Glu Met Leu Pro
      65                      70                      75                      80

Pro Asp Val Arg Val Ala Arg Asp Thr Gln Asp Leu Leu Val Glu Cys
      85                      90                      95
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Cys Val Glu Phe Ile Asn Leu Leu Ser Ser Glu Ser Asn Asp Val Cys
 100 105 110
 Ser Arg Asp Asp Lys Lys Thr Ile Ala Pro Glu His Val Ile Arg Ala
 115 120 125
 Leu Gln Asp Leu Gly Phe Lys Glu Tyr Val Glu Glu Val Tyr Ala Ala
 130 135 140
 Tyr Glu Gln His Lys Leu Glu Thr Leu Asp Ser Pro Lys Ala Thr Lys
 145 150 155 160
 Phe Thr Gly Ile Glu Met Thr Glu Glu Glu Ala Val Ala Glu Gln Gln
 165 170 175
 Arg Met Phe Ala Glu Ala Arg Ala Arg Met Asn Asn Gly Ala Ala Lys
 180 185 190
 Pro Lys Glu Pro Ala Leu Glu Pro Gln Asn Gln Pro Gln Gln Pro Pro
 195 200 205
 Gln Pro His Leu Gln Leu His Pro Gln Ala Gln Gln Pro Pro Gln Pro
 210 215 220
 Gln Pro Gln Leu His His Pro Gln Ser Gln Gln Pro Leu His Pro Gln
 225 230 235 240
 Leu Gln Pro Tyr Thr Gln Ala Pro Pro Gln Gln Pro Leu His Pro Gln
 245 250 255
 Leu Gln Pro Tyr Thr Gln Ala Pro Pro Gln Gln Pro Leu Gln Pro Pro
 260 265 270
 Leu Gln Leu Tyr Pro Gln Ala Gln Pro Glu Gln Pro Leu Gln Pro Gln
 275 280 285
 Ser Ser Gly Ser Thr Thr Gly Thr Cys Val Ile Ser Thr Ala Ala Pro
 290 295 300
 Ser Ala Thr Gly Thr Thr Ala Ala Ala Thr Ser Ala Pro Ala Ile Pro
 305 310 315 320
 Ala Ile Ser Thr Ala Ala Pro Ser Ala Thr Pro Ala Asp Ala Ser Ala
 325 330 335
 Ala Ala Ala Ala Ala Ala Thr Ser Thr Pro Ala Thr
 340 345

<210> 21
 <211> 1288
 <212> DNA
 <213> Triticum aestivum

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 gggcaagtcc aaggaggacg tctccctccc caaatcaaca atgaccaaga ttatcaagga 120
 gatgctaccg cctgatgttc gtagtagcaag agatacacag gatcttcttg ttgaatgctg 180
 tgtagagttc atcaatcttc tttcttcgga atccaatgac gtgtgcagcc gggacgacaa 240

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gaaaactatt gccctgaac atgttattag ggctttgcag gatcttggt tcaaggagta 300
tggtgaagaa gtttatgcag cctacgaaca gcacaagctt gaaactctgg actctccaaa 360
agcaaccaag ttactggta tagagatgac tgaagaagaa gctgttgctg aacagcagag 420
aatgtttgct gaagcccag caaggatgaa caatggagct gccaaaccaa aggagcctgc 480
attagaacca cagaatcaac cccaacagcc cccacaacct catctgcagc tgcattccca 540
agcacagcag cctccacaac ctcaaccgca actgcattat cctcaatcac agcagcccct 600
gcaaccggtt actcaggctc caccacagca acccctgcat cctcaactgc aacagtatac 660
tcaggctcca ccacagcaac ccctacaacc tccactgcag ctgtatcctc aggctcaacc 720
tgagcaaccg ctgcagcctc aatcctcagg atcaaccaca ggaacctgtg taatctcagc 780
tgcagctcca tctgcaaccg gcacactgct gctgcaacct ccgcccagc aatccccgca 840
atctcaactg cagctccatc agcaacccca gccgacgcta gtgccgccgc cgcaacctca 900
accccagcca cttgaactgc agcagcccca gccgctaaca caactgcaag cggaacatgg 960
cctggactgg gacagttagt ggttcggaac atgtagcgtc actataagtt aagactctgc 1020
ctcctttaa attgtgcgtt aggtttgcct gcatcttgta caatgtaa atcggtgtgat 1080
ttcagccacc gtgtctaata atctgaagct ctctagtaag cgatgtactt actgcgctgg 1140
gtactgtgtt tatgactgct gtagtctcat ggtattgtgt gtgacgtgtc agaagctact 1200
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1288

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<210> 22
 <211> 312
 <212> PRT
 <213> Triticum aestivum

<400> 22
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 Pro Lys Ser Thr Met Thr Lys Ile Ile Lys Glu Met Leu Pro Pro Asp
 20 25 30
 Val Arg Val Ala Arg Asp Thr Gln Asp Leu Leu Val Glu Cys Cys Val
 35 40 45
 Glu Phe Ile Asn Leu Leu Ser Ser Glu Ser Asn Asp Val Cys Ser Arg
 50 55 60
 Asp Asp Lys Lys Thr Ile Ala Pro Glu His Val Ile Arg Ala Leu Gln
 65 70 75 80
 Asp Leu Gly Phe Lys Glu Tyr Val Glu Glu Val Tyr Ala Ala Tyr Glu
 85 90 95
 Gln His Lys Leu Glu Thr Leu Asp Ser Pro Lys Ala Thr Lys Phe Thr
 100 105 110
 Gly Ile Glu Met Thr Glu Glu Glu Ala Val Ala Glu Gln Gln Arg Met
 115 120 125
 Phe Ala Glu Ala Arg Ala Arg Met Asn Asn Gly Ala Ala Lys Pro Lys
 130 135 140
 Glu Pro Ala Leu Glu Pro Gln Asn Gln Pro Gln Gln Pro Pro Gln Pro
 145 150 155 160
 His Leu Gln Leu His Pro Gln Ala Gln Gln Pro Pro Gln Pro Gln Pro
 165 170 175
 Gln Leu His Tyr Pro Gln Ser Gln Gln Pro Leu Gln Pro Phe Thr Gln

180 185 190

Ala Pro Pro Gln Gln Pro Leu His Pro Gln Leu Gln Gln Tyr Thr Gln
195 200 205

Ala Pro Pro Gln Gln Pro Leu Gln Pro Pro Leu Gln Leu Tyr Pro Gln
210 215 220

Ala Gln Pro Glu Gln Pro Leu Gln Pro Gln Ser Ser Gly Ser Thr Thr
225 230 235 240

Gly Thr Cys Val Ile Ser Ala Ala Ala Pro Ser Ala Thr Gly Thr Leu
245 250 255

Leu Leu Gln Pro Pro Pro Gln Gln Ser Pro Gln Ser Gln Leu Gln Leu
260 265 270

His Gln Gln Pro Gln Pro Thr Leu Val Pro Pro Pro Gln Pro Gln Pro
275 280 285

Gln Pro Leu Glu Leu Gln Gln Pro Gln Pro Leu Thr Gln Leu Gln Ala
290 295 300

Glu His Gly Leu Asp Trp Asp Ser
305 310

<210> 23
<211> 1001
<212> DNA
<213> Zea mays

<400> 23

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tttcgaggtc	tcttgaattg	tttttacaag	atttaattga	ccgtacttat	gaaattactc	180
ttcaaaagtgg	agcaaagaca	ctgaattcct	tccacctgaa	gcaatgtgtg	aagaggtaca	240
gttcttttga	tttcctaact	gaagttgtca	gcaaggtacc	agatcttggt	ggcgctgatt	300
cctgtggaga	tgaaagagga	ttacctagaa	gaagaaagtc	aaatggcagt	gacccagaga	360
atgatgaatc	aagatctagt	aaaatggcca	taagaaatgc	aaacatcagc	cccagaggaa	420
cgtgggaggg	gtcgaggcag	aggacgaggt	cggccaccaa	ccaagagaaa	ggaggttggt	480
tatgtacaat	ttgaagatga	gagcagcatg	tttgctgaac	aaggtgagcc	cttgccagga	540
gaggaaacag	ttcaagagat	caatggcaac	gagaccatgc	ctcaaagcac	gcaacctcca	600
gtagagtccg	ccaacagccc	ttgcacaagc	tacaacaagt	tctaaggcgg	aagaagcgaa	660
cagtgatcat	cagtcagatt	ggcctatgcc	agatgccatt	ggaagcatcg	gtgtcgtgcc	720
atctggtttt	ggacatctga	cagtgcaggt	tgaagatgag	gactacgaca	atgaggatta	780
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atatagtttg	aaatagttgc	cgcagtttac	ctgtgattgt	ctgtcgtttt	atgcggttat	900
gtagtcctgt	gtaactttcg	ttctccaata	attgcttggt	agttgctttt	ttacatgatt	960
caagtgtttt	gtgacaaaaa	aaaaaaaaaa	aaaaaaaaaa	a		1001

<210> 24
<211> 158
<212> PRT
<213> Zea mays

<400> 24

Met	Arg	Lys	Lys	Leu	Gly	Thr	Arg	Phe	Pro	Ala	Ala	Arg	Ile	Lys	Lys
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Ile Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro
 20 25 30
 Val Leu Val Ser Arg Ser Leu Glu Leu Phe Leu Gln Asp Leu Ile Asp
 35 40 45
 Arg Thr Tyr Glu Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn Ser
 50 55 60
 Phe His Leu Lys Gln Cys Val Lys Arg Tyr Ser Ser Phe Asp Phe Leu
 65 70 75 80
 Thr Glu Val Val Ser Lys Val Pro Asp Leu Gly Gly Ala Asp Ser Cys
 85 90 95
 Gly Asp Glu Arg Gly Leu Pro Arg Arg Arg Lys Ser Asn Gly Ser Asp
 100 105 110
 Pro Glu Asn Asp Glu Ser Arg Ser Ser Lys Met Ala Ile Arg Asn Ala
 115 120 125
 Asn Ile Ser Pro Arg Gly Thr Trp Glu Gly Ser Arg Gln Arg Thr Arg
 130 135 140
 Ser Ala Thr Asn Gln Glu Lys Gly Gly Trp Leu Cys Thr Ile
 145 150 155

<210> 25
 <211> 562
 <212> DNA
 <213> Zea mays

<220>
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 <222> (402)
 <223> n=a,c,g or t

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 <222> (419)
 <223> n=a,c,g or t

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 <222> (439)
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<220>
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 <222> (459)

<223> n=a,c,g or t

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<221> unsure

<222> (500)

<223> n=a,c,g or t

<220>

<221> unsure

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<222> (509)

<223> n=a,c,g or t

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<221> unsure

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<223> n=a,c,g or t

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<221> unsure

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<221> unsure

<222> (542)

<223> n=a,c,g or t

<400> 25

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gattgcatta gcagtgcctg ttttagtctc gagggctctt gaattgtttt tacaagattt 180
aattgaccgg acttatgaaa ttactcttca aagtggagca aagacactga attccttcca 240
cctgaagcaa tgtgtgaaga ggtacagttc ttttgatttc ctaactgaat tgtcagcaag 300
taccagatct tgggtggtgct gatcatgtgg agatgaaaga gtgttactag aagaagaaat 360
caaatggcat gaccagagaa tgataatcaa atcagtaaat gntatagaaa tcaatacanc 420

canagactgg aggggtcagna angcaagcgc acaccagana agattgtact cattaaataa 480
cacagttcga cagggaactn cagnaggana tcanttanan gacantaccc aanagnactg 540
cnaacctgca gtaatcaggg aa 562

<210> 26
<211> 86
<212> PRT
<213> Zea mays

<400> 26
Met Arg Lys Lys Leu Gly Thr Arg Phe Pro Ala Ala Arg Ile Lys Lys
1 5 10 15
Ile Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro
20 25 30
Val Leu Val Ser Arg Ala Leu Glu Leu Phe Leu Gln Asp Leu Ile Asp
35 40 45
Arg Thr Tyr Glu Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn Ser
50 55 60
Phe His Leu Lys Gln Cys Val Lys Arg Tyr Ser Ser Phe Asp Phe Leu
65 70 75 80
Thr Glu Leu Ser Ala Ser
85

<210> 27
<211> 1055
<212> DNA
<213> Zea mays

<400> 27
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gattgcatta gcagtgcctg ttttagtctc gagggctctt gaattgtttt tacaagattt 180
aattgaccgg acttatgaaa ttactcttca aagtggagca aagacactga attccttcca 240
cctgaagcaa tgtgtgaaga ggtacagttc ttttgatttc ctaactgaag ttgtcagcaa 300
ggtaccagat cttggtggtg ctgattcatg tggagatgaa agagtgttac ctagaagaag 360
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accaaccaag agaaaggaag ttggttacgt acaatttgaa gatgagagca gcatgtttgc 540
tgaacaagggt gaaaccttac caggagaggg aacagttcca gagatcaaca gcggcaacga 600
gattacgcct caaagcacgc aacctccgct aacagcccct gcgcaagcta caaattctaa 660
ggtggaagaa gcaagcaccg atcatcagtc agattggcct atgccagatg ccactggaaa 720
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tggtgttgta aaatgtaaat atagcttgaa gtagctgccg cagcttagct atgattgtct 900
gttatgaggt tatgtagtgt ccctgtgtaa ctctgtaat tgcttttttag ttgccttttc 960
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tcgactatatt ctaagtaaaa aaaaaaaaaa aaaaaa 1055

<210> 28
<211> 251
<212> PRT
<213> Zea mays

<400> 28

Met Arg Lys Lys Leu Gly Thr Arg Phe Pro Ala Ala Arg Ile Lys Lys
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Ile Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro
20 25 30

Val Leu Val Ser Arg Ala Leu Glu Leu Phe Leu Gln Asp Leu Ile Asp
35 40 45

Arg Thr Tyr Glu Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn Ser
50 55 60

Phe His Leu Lys Gln Cys Val Lys Arg Tyr Ser Ser Phe Asp Phe Leu
65 70 75 80

Thr Glu Val Val Ser Lys Val Pro Asp Leu Gly Gly Ala Asp Ser Cys
85 90 95

Gly Asp Glu Arg Val Leu Pro Arg Arg Arg Lys Ser Asn Gly Ser Asp
100 105 110

Pro Glu Asn Asp Glu Ser Arg Ser Ser Lys Met Ala Ile Arg Asn Ala
115 120 125

Asn Thr Ser Pro Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly
130 135 140

Arg Pro Pro Thr Lys Arg Lys Glu Val Gly Tyr Val Gln Phe Glu Asp
145 150 155 160

Glu Ser Ser Met Phe Ala Glu Gln Gly Glu Thr Leu Pro Gly Glu Gly
165 170 175

Thr Val Pro Glu Ile Asn Ser Gly Asn Glu Ile Thr Pro Gln Ser Thr
180 185 190

Gln Pro Pro Leu Thr Ala Pro Ala Gln Ala Thr Asn Ser Lys Val Glu
195 200 205

Glu Ala Ser Thr Asp His Gln Ser Asp Trp Pro Met Pro Asp Ala Thr
210 215 220

Gly Asn Ile Gly Val Gly Pro Ser Gly Phe Gly His Leu Thr Val Gln
225 230 235 240

Val Asp Glu Asp Glu Asp Tyr Asp Asn Glu Asp
245 250

<210> 29

<211> 543

<212> DNA

<213> Oryza sp.

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<222> (388)

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<222> (514)
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<222> (516)
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gacgttggca agattgcact agctgtacct gttttagtat cgagggccct tgaattgttt 180
ttgcaagatt taattgaccg aacttacgaa attacactgc aaagtgggtgc aaagacattg 240
aattccttcc acctaaagca atgtgtgagg aggtacattc ttttgacttc ctaactgagt 300
tgtcaacaag gtaccggacc tcggtggcgc tgaccatgtg gagatgatag agcattaccc 360
agaagaagaa aaccttgcca aatggaantg ccannagaat gaggatccca tnaagcnaat 420
ggccttaaga atgcaaatac atcccanagg acttgganaa gccaaagtana ggcaaggaca 480
cancacaanc gaaggattgt aagtcattna ggtnanacac atttgcgata gggcaaccta 540
cag 543

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<210> 30
<211> 71
<212> PRT
<213> Oryza sp.

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Met Arg Lys Lys Leu Gly Thr Arg Phe Pro Ala Ala Arg Ile Lys Lys
 1             5             10             15

Ile Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro
             20             25             30

Val Leu Val Ser Arg Ala Leu Glu Leu Phe Leu Gln Asp Leu Ile Asp
 35             40             45

Arg Thr Tyr Glu Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn Ser
 50             55             60

Phe His Leu Lys Gln Cys Val
 65             70

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<210> 31
<211> 1024
<212> DNA
<213> Oryza sativa

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<400> 31
ctgcgatagc gtggaggagc ggaggcggag gcgaacgcga ggaggaagac gaagatgagg 60
aagaagctgg gcacccgctt ccccgcgga cggatcaaaa agatcatgca ggctgatgag 120
gacgttggca agattgcact agctgtacct gttttagtat cgagggccct tgaattgttt 180
ttgcaagatt taattgaccg aacttacgaa attacactgc aaagtgggtgc aaagacattg 240
aattccttcc acctaaagca atgtgtgagg aggtacagtt cttttgactt cctaactgag 300
gttgtcaaca aggtaccgga cctcggtggc gctgactcat gtggagatga tagagcatta 360
cccagaagaa gaaaagcctt gccaaatgga agtgaccag agaatgagga atctcgatca 420
agcaaaatgg ccgtaagaag tgcaaatac agtcccagag gacgtgggag aggtcgaggt 480
agagggcgag gacgaccacc caccaagcgg aaggaagttg gttatgtaca atttgaggat 540
gagagcagca tgtttgctga tcagggcgaa gccttaccag gagaggagac ggttccagag 600
accatccatg gcaccgagag cgtacctcca agcacacacc ctccagcaga agccccatcg 660
gcagcagaga taccagctcc aaatccaaag gtggaagaag cgaaaaacga cgaccatcag 720
ccggtattggc ctatgccaga tgcgattgga aacatcggtg tcggaccatc cggttttgga 780
catcttacgg tgcaagttga cgaggatgag gactacgaca acgaggatta gccacggcca 840
tcttctgatt gttatgcact aacagggcag ttctcctggt gttgtaaaaat gtaaatatgt 900
agctgcagct agctgtgatg tgctgctgat gtaatgcagt atgtagttgt cccgtgtaac 960
tttgtctgtt ttccaataat tgcttgctag ttgcctcaca ttgttgaaaa aaaaaaaaaa 1020
aaaa 1024

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<210> 32
 <211> 258
 <212> PRT
 <213> Oryza sativa

<400> 32

Met	Arg	Lys	Lys	Leu	Gly	Thr	Arg	Phe	Pro	Ala	Ala	Arg	Ile	Lys	Lys
1				5					10					15	
Ile	Met	Gln	Ala	Asp	Glu	Asp	Val	Gly	Lys	Ile	Ala	Leu	Ala	Val	Pro
			20					25					30		
Val	Leu	Val	Ser	Arg	Ala	Leu	Glu	Leu	Phe	Leu	Gln	Asp	Leu	Ile	Asp
		35					40					45			
Arg	Thr	Tyr	Glu	Ile	Thr	Leu	Gln	Ser	Gly	Ala	Lys	Thr	Leu	Asn	Ser
	50					55					60				
Phe	His	Leu	Lys	Gln	Cys	Val	Arg	Arg	Tyr	Ser	Ser	Phe	Asp	Phe	Leu
65					70					75					80
Thr	Glu	Val	Val	Asn	Lys	Val	Pro	Asp	Leu	Gly	Gly	Ala	Asp	Ser	Cys
				85					90					95	
Gly	Asp	Asp	Arg	Ala	Leu	Pro	Arg	Arg	Arg	Lys	Ala	Leu	Pro	Asn	Gly
			100					105					110		
Ser	Asp	Pro	Glu	Asn	Glu	Glu	Ser	Arg	Ser	Ser	Lys	Met	Ala	Val	Arg
		115					120					125			
Ser	Ala	Asn	Ile	Ser	Pro	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly
	130					135					140				
Arg	Gly	Arg	Pro	Pro	Thr	Lys	Arg	Lys	Glu	Val	Gly	Tyr	Val	Gln	Phe
145					150					155					160
Glu	Asp	Glu	Ser	Ser	Met	Phe	Ala	Asp	Gln	Gly	Glu	Ala	Leu	Pro	Gly
				165					170					175	
Glu	Glu	Thr	Val	Pro	Glu	Thr	Ile	His	Gly	Thr	Glu	Ser	Val	Pro	Pro
			180					185					190		
Ser	Thr	His	Pro	Pro	Ala	Glu	Ala	Pro	Ser	Ala	Ala	Glu	Ile	Pro	Ala
		195				200						205			
Pro	Asn	Pro	Lys	Val	Glu	Glu	Ala	Lys	Asn	Asp	Asp	His	Gln	Pro	Asp
	210					215					220				
Trp	Pro	Met	Pro	Asp	Ala	Ile	Gly	Asn	Ile	Gly	Val	Gly	Pro	Ser	Gly
225					230					235					240
Phe	Gly	His	Leu	Thr	Val	Gln	Val	Asp	Glu	Asp	Glu	Asp	Tyr	Asp	Asn
				245					250					255	

Glu Asp

<210> 33
 <211> 1274

<212> DNA
 <213> Glycine max

<400> 33

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ctgaaatgag tttcttcgat ttcacccctgt tgatgatagg gtcgctcttt ctgttcaaag 60
ctttcgattt tactttcttg gtctccttct tctgcttctt ttgattcccc caattcttca 120
gctttcaaaa ccctaattctg ctgccatgag gaagaagctc gataccggtt tccctgctgc 180
tcggataaag aagataatgc aagctgatga ggatgttgga aagatagcac tcgctgtgcc 240
tgtttttagtt tctaaagctc tagaactatt tttgcaagat ctttgtgacc gcacttatga 300
aataactctt caaagaggag caaagaccat gaattcattg catttaaaac attgtgtaca 360
aagctataat gtctttgact ttctgaggga cgttgtttagc agggttcctg actacagcca 420
tggccatggc catgctgagg ctggtcctga tgatcgggcc attgcaaaaa gaaggaaagc 480
tgttggtgat gatggtaatg acagtgatga agaggctaag aggagcaaga tgcattgatt 540
gggccacact ggcagtactg gtaggggaag aggccgaggt agaggaagag gccgtggccg 600
agggcgacca cctttaaata gagagatata tcatcaggat gctgaatctg agccttgcac 660
ttctgttcag ccaagcaacc cacaaaatac aaacacaagt gttgcaatgg atagtggttc 720
tgagtcaaag gaaataccaa aggagcagaa cattgcagtt cctgttgaaa gcactgattc 780
gctccggaac atcgatctga atgccattac gaatgaaaat gatgacaaaa aggctagcgc 840
agcagcggat gcctctgtgc ctgaacctga tgcctctgtg cctgaacctc caacagagag 900
caagcatgaa gaaattccag ggtggtctct ttctgatgtg gacaagatgg ccattgattc 960
gctgcagctt gcacaacttg gtaggccact agaagaggat gaagaagact atgatgaaga 1020
ggaggggtaa atattattag tctttggtga ttagattagt gaaaagctca tcatgataac 1080
tgtagaataa gtacatacta gtgttatgat tatgagtatc cactagctgt caatgcatgt 1140
accatgttgg ctgaagaaag gatctgaatg ccccttttca ttaatctgct ttgtatgtgt 1200
agctgatgta tcttttcctt gaccagtaat gttagtttcg tgtactttta ggcctaaaaa 1260
aaaaaaaaaa aaaa 1274

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<210> 34
 <211> 294
 <212> PRT
 <213> Glycine max

<400> 34

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Met Arg Lys Lys Leu Asp Thr Arg Phe Pro Ala Ala Arg Ile Lys Lys
 1          5          10          15

Ile Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro
          20          25          30

Val Leu Val Ser Lys Ala Leu Glu Leu Phe Leu Gln Asp Leu Cys Asp
          35          40          45

Arg Thr Tyr Glu Ile Thr Leu Gln Arg Gly Ala Lys Thr Met Asn Ser
          50          55          60

Leu His Leu Lys His Cys Val Gln Ser Tyr Asn Val Phe Asp Phe Leu
          65          70          75          80

Arg Asp Val Val Ser Arg Val Pro Asp Tyr Ser His Gly His Gly His
          85          90          95

Ala Glu Ala Gly Pro Asp Asp Arg Ala Ile Ala Lys Arg Arg Lys Ala
          100          105          110

Val Gly Asp Asp Gly Asn Asp Ser Asp Glu Glu Ala Lys Arg Ser Lys
          115          120          125

Met His Glu Leu Gly His Thr Gly Ser Thr Gly Arg Gly Arg Gly Arg
          130          135          140

```


Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Pro Pro Leu Asn Arg Glu
 145 150 155 160
 Ile Tyr His Gln Asp Ala Glu Ser Glu Pro Cys Thr Ser Val Gln Pro
 165 170 175
 Ser Asn Pro Gln Asn Thr Asn Thr Ser Val Ala Met Asp Ser Gly Ser
 180 185 190
 Glu Ser Lys Glu Ile Pro Lys Glu Gln Asn Ile Ala Val Pro Val Glu
 195 200 205
 Ser Thr Asp Ser Leu Arg Asn Ile Asp Leu Asn Ala Ile Thr Asn Glu
 210 215 220
 Asn Asp Asp Lys Lys Ala Ser Ala Ala Ala Asp Ala Ser Val Pro Glu
 225 230 235 240
 Pro Asp Ala Ser Val Pro Glu Pro Pro Thr Glu Ser Lys His Glu Glu
 245 250 255
 Ile Pro Gly Trp Ser Leu Ser Asp Val Asp Lys Met Ala Ile Asp Ser
 260 265 270
 Leu Gln Leu Ala Gln Leu Gly Arg Pro Leu Glu Glu Asp Glu Glu Asp
 275 280 285
 Tyr Asp Glu Glu Glu Gly
 290

<210> 35
 <211> 534
 <212> DNA
 <213> Triticum sp.

<220>
 <221> unsure
 <222> (441)
 <223> n=a,c,g or t

<400> 35
 gttccccgcg gcacggatca aaaagataat gcaagcagat gaggatgttg gcaaaattgc 60
 actggctgtg cctgttttag ttctgagagc ccttgaattg tttctgcaag atttgatcga 120
 ccactcatac aaaattactc ttcaaagtgg tgcaaagaca ctgaattcct tccacctaaa 180
 gcaatgtgtg aagaggtaca gctcttttga ctctctaact gagattgtca acaaggtgcc 240
 agatctcggt ggcggtgaat cttgtggaga tgaaagagga ttaccagaa gaaggaaatt 300
 ttcaaattgga agcgaccagc agaatgagga gcccgatct agcaaaatgc ccataagaag 360
 cttgaacacc agtcccagag gacgaggcag aggtcgagga agagggcgag ggcggcctcc 420
 aaaccaagag aaaggaaatt ngttatgtac agtttgagga tgagagcagc atgtttgctg 480
 aacaaagtga acccttgcca ggagattgag atagtcccg agaccaaccg tggc 534

<210> 36
 <211> 151
 <212> PRT
 <213> Triticum sp.

<220>
 <221> UNSURE

<222> (147)
<223> Xaa=ANY AMINO ACID

<400> 36
Phe Pro Ala Ala Arg Ile Lys Lys Ile Met Gln Ala Asp Glu Asp Val
1 5 10 15
Gly Lys Ile Ala Leu Ala Val Pro Val Leu Val Ser Arg Ala Leu Glu
20 25 30
Leu Phe Leu Gln Asp Leu Ile Asp His Ser Tyr Lys Ile Thr Leu Gln
35 40 45
Ser Gly Ala Lys Thr Leu Asn Ser Phe His Leu Lys Gln Cys Val Lys
50 55 60
Arg Tyr Ser Ser Phe Asp Phe Leu Thr Glu Ile Val Asn Lys Val Pro
65 70 75 80
Asp Leu Gly Gly Gly Glu Ser Cys Gly Asp Glu Arg Gly Leu Pro Arg
85 90 95
Arg Arg Lys Phe Ser Asn Gly Ser Asp Pro Glu Asn Glu Glu Pro Arg
100 105 110
Ser Ser Lys Met Pro Ile Arg Ser Leu Asn Thr Ser Pro Arg Gly Arg
115 120 125
Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Pro Pro Asn Gln Glu Lys
130 135 140
Gly Asn Xaa Leu Cys Thr Val
145 150

<210> 37
<211> 458
<212> DNA
<213> Triticum sp.

<220>
<221> unsure
<222> (216)
<223> n=a,c,g or t

<220>
<221> unsure
<222> (242)
<223> n=a,c,g or t

<220>
<221> unsure
<222> (256)
<223> n=a,c,g or t

<220>
<221> unsure
<222> (266)
<223> n=a,c,g or t

<220>
 <221> unsure
 <222> (275)
 <223> n=a,c,g or t

<220>
 <221> unsure
 <222> (295)
 <223> n=a,c,g or t

<220>
 <221> unsure
 <222> (311)
 <223> n=a,c,g or t

<220>
 <221> unsure
 <222> (314)
 <223> n=a,c,g or t

<220>
 <221> unsure
 <222> (335)
 <223> n=a,c,g or t

<220>
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 <222> (339)
 <223> n=a,c,g or t

<220>
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 <222> (345)
 <223> n=a,c,g or t

<220>
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 <222> (351)
 <223> n=a,c,g or t

<220>
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 <222> (355)
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<220>
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<220>
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 <222> (379)
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<220>
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 <222> (400)
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<220>
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 <222> (410)
 <223> n=a,c,g or t

<220>
 <221> unsure
 <222> (434)
 <223> n=a,c,g or t

<220>
 <221> unsure
 <222> (447)
 <223> n=a,c,g or t

<220>
 <221> unsure
 <222> (448)
 <223> n=a,c,g or t

<220>
 <221> unsure
 <222> (449)
 <223> n=a,c,g or t

<400> 37
 gaggaagaag ctgggcaccc ggttccccgc ggcacggatc aaaaagataa tgcaagcaga 60
 tgaggatggt ggcaaaattg cactggctgt gcctgtttta gtttcgagag cccttgaatt 120
 gtttctgcaa gatttgatcg accactcata caaaattact cttcaaagtgt gtgcaaagac 180
 actgaattcc ttccacctaa agcaatgtgt gaagangtac agctcttttg acttcctaac 240
 tnagattgtc aacaangtgc caaatntccg tggcnggtta atcttggttg agatnaaaga 300
 ggattaccca naanaaggaa atttttaaatt ggaancganc caaanaatga nggancccga 360
 ttttaacaaaa tgccatnana aacttgaaca ccattccaan aggacaaggn aaaggtccag 420
 gaaaaggcaa gggnggctcc aaccaannna aaggaatt 458

<210> 38
 <211> 91
 <212> PRT
 <213> Triticum sp.

<220>
 <221> UNSURE
 <222> (72)
 <223> Xaa=ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (81)
 <223> Xaa=ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (85)
 <223> Xaa=ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (89)
 <223> Xaa=ANY AMINO ACID

<400> 38
 Arg Lys Lys Leu Gly Thr Arg Phe Pro Ala Ala Arg Ile Lys Lys Ile
 1 5 10 15
 Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro Val
 20 25 30
 Leu Val Ser Arg Ala Leu Glu Leu Phe Leu Gln Asp Leu Ile Asp His
 35 40 45
 Ser Tyr Lys Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn Ser Phe
 50 55 60
 His Leu Lys Gln Cys Val Lys·Xaa Tyr Ser Ser Phe Asp Phe Leu Thr
 65 70 75 80
 Xaa Ile Val Asn Xaa Val Pro Asn Xaa Arg Gly
 85 90

<210> 39
 <211> 950
 <212> DNA
 <213> Triticum aestivum

<400> 39
 gcacgaggag gaagaagctg ggcacccggt tccccgcggc acggatcaaa aagataatgc 60
 aagcagatga ggatgttggc aaaattgcac tggctgtgcc tgttttagtt tcgagagccc 120
 ttgaattggt tctgcaagat ttgatcgacc actcatacaa aattactctt caaagtgggtg 180
 caaagacact gaattccttc cacctaaagc aatgtgtgaa gaggtacagc tcttttgact 240
 tcctaactga gattgtcaac aaggtgccag atctcgggtg cggatgaatct tgtggagatg 300
 aaagaggatt acccagaaga aggaaatttt caaatggaag cgacccagag aatgaggagc 360
 cccgatctag caaaatgccc ataagaagct tgaacaccag tcccagagga cgaggcagag 420
 gtcgaggaag agggcgaggg cggcctccaa ccaagagaaa ggaaattggt tatgtacagt 480
 ttgaggatga gagcagcatg tttgctgaac aaagtgaacc cttgccagga gatgagatag 540
 ttccggagac caaccgtggc aatgagagta ttcccaaaag ctcacatcct ctagtggagg 600
 ctccatcagc catgacgcca gctgtgattt caaaggttga agaagctagc accaaccatc 660
 agccagattg gcctatgcca gatgccattg gaggcattgg tgttggaaca tccagttttg 720
 gacatctgac agtgcagggt gatgaggtag aggactacga caatgaggat taggcatagt 780
 catcctctca ttcacatcat gctctaacag gacagttctc ctggtgttgt acattgtaaa 840
 tattgtttca agtagttact gcagctatga tgtgtaacct atttcttttt cccaataatt 900
 ggttctgagt tgccgcattg ttgacctaaa aaaaaaaaaa aaaaaaaaaa 950

<210> 40
 <211> 256
 <212> PRT
 <213> Triticum aestivum

<400> 40
 Thr Arg Arg Lys Lys Leu Gly Thr Arg Phe Pro Ala Ala Arg Ile Lys
 1 5 10 15
 Lys Ile Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val
 20 25 30
 Pro Val Leu Val Ser Arg Ala Leu Glu Leu Phe Leu Gln Asp Leu Ile
 35 40 45
 Asp His Ser Tyr Lys Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn

50	55	60
Ser Phe His Leu Lys Gln Cys Val Lys Arg Tyr Ser Ser Phe Asp Phe		
65	70	75 80
Leu Thr Glu Ile Val Asn Lys Val Pro Asp Leu Gly Gly Gly Glu Ser		
	85	90 95
Cys Gly Asp Glu Arg Gly Leu Pro Arg Arg Arg Lys Phe Ser Asn Gly		
	100	105 110
Ser Asp Pro Glu Asn Glu Glu Pro Arg Ser Ser Lys Met Pro Ile Arg		
	115	120 125
Ser Leu Asn Thr Ser Pro Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly		
	130	135 140
Arg Gly Arg Pro Pro Thr Lys Arg Lys Glu Ile Gly Tyr Val Gln Phe		
	145	150 155 160
Glu Asp Glu Ser Ser Met Phe Ala Glu Gln Ser Glu Pro Leu Pro Gly		
	165	170 175
Asp Glu Ile Val Pro Glu Thr Asn Arg Gly Asn Glu Ser Ile Pro Gln		
	180	185 190
Ser Ser His Pro Leu Val Glu Ala Pro Ser Ala Met Thr Pro Ala Val		
	195	200 205
Ile Ser Lys Val Glu Glu Ala Ser Thr Asn His Gln Pro Asp Trp Pro		
	210	215 220
Met Pro Asp Ala Ile Gly Gly Ile Gly Val Gly Pro Ser Ser Phe Gly		
	225	230 235 240
His Leu Thr Val Gln Val Asp Glu Val Glu Asp Tyr Asp Asn Glu Asp		
	245	250 255

<210> 41

<211> 159

<212> PRT

<213> Arabidopsis thaliana

<400> 41

Met Asp Pro Met Asp Ile Val Gly Lys Ser Lys Glu Asp Ala Ser Leu
1 5 10 15

Pro Lys Ala Thr Met Thr Lys Ile Ile Lys Glu Met Leu Pro Pro Asp
20 25 30

Val Arg Val Ala Arg Asp Ala Gln Asp Leu Leu Ile Glu Cys Cys Val
35 40 45

Glu Phe Ile Asn Leu Val Ser Ser Glu Ser Asn Asp Val Cys Asn Lys
50 55 60

Glu Asp Lys Arg Thr Ile Ala Pro Glu His Val Leu Lys Ala Leu Gln
65 70 75 80

Val Leu Gly Phe Gly Glu Tyr Ile Glu Glu Val Tyr Ala Ala Tyr Glu
85 90 95
Gln His Lys Tyr Glu Thr Met Gln Asp Thr Gln Arg Ser Val Lys Trp
100 105 110
Asn Pro Gly Ala Gln Met Thr Glu Glu Glu Ala Ala Ala Glu Gln Gln
115 120 125
Arg Met Phe Ala Glu Ala Arg Ala Arg Met Asn Gly Gly Val Ser Val
130 135 140
Pro Gln Pro Glu His Pro Glu Thr Asp Gln Arg Ser Pro Gln Ser
145 150 155

<210> 42
<211> 205
<212> PRT
<213> Homo sapiens

<400> 42
Met Pro Ser Lys Lys Lys Lys Tyr Asn Ala Arg Phe Pro Pro Ala Arg
1 5 10 15
Ile Lys Lys Ile Met Gln Thr Asp Glu Glu Ile Gly Lys Val Ala Ala
20 25 30
Ala Val Pro Val Ile Ile Ser Arg Ala Leu Glu Leu Phe Leu Glu Ser
35 40 45
Leu Leu Lys Lys Ala Cys Gln Val Thr Gln Ser Arg Asn Ala Lys Thr
50 55 60
Met Thr Thr Ser His Leu Lys Gln Cys Ile Glu Leu Glu Gln Gln Phe
65 70 75 80
Asp Phe Leu Lys Asp Leu Val Ala Ser Val Pro Asp Met Gln Gly Asp
85 90 95
Gly Glu Asp Asn His Met Asp Gly Asp Lys Gly Ala Arg Arg Gly Arg
100 105 110
Lys Pro Gly Ser Gly Gly Arg Lys Asn Gly Gly Met Gly Thr Lys Ser
115 120 125
Lys Asp Lys Lys Leu Ser Gly Thr Asp Ser Glu Gln Glu Asp Glu Ser
130 135 140
Glu Asp Thr Asp Thr Asp Gly Glu Glu Glu Thr Ser Gln Pro Pro Pro
145 150 155 160
Gln Ala Ser His Pro Ser Ala His Phe Gln Ser Pro Pro Thr Pro Phe
165 170 175
Leu Pro Phe Ala Ser Thr Leu Pro Leu Pro Pro Ala Pro Pro Gly Pro
180 185 190
Ser Ala Pro Asp Glu Glu Asp Glu Glu Asp Tyr Asp Ser
195 200 205

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 43
gttgctcagc tacagcttgt tcc

23

<210> 44
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 44
ttggagaatc cagggtatca tgc

23

<210> 45
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<220>
<221> modified_base
<222> (24)..(25)
<223> i

<220>
<221> modified_base
<222> (29)..(30)
<223> i

<220>
<221> modified_base
<222> (34)..(35)
<223> i

<400> 45
ggccacgcgt cgactagtagt gggnnngggnn gggnnng

36

<210> 46
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic

Oligonucleotide

<400> 46
caagtcgacg gccgcttgaa cctcttc 27

<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 47
cttataactga ggctacacaa c 21

<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 48
ataccgggt gaactgtcca agccatgttc 30

<210> 49
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 49
gttaggtgtc ggcctggag a 21

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 50
taagaattca tggatccgat ggatatcgtg 30

<210> 51
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic

Oligonucleotide

<400> 51
cgggatccga tagtgggatt gtgcgtc 27

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 52
actggctcac gctaggaacc 20

<210> 53
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 53
gccagcttc ttcccatgg cttcgtcttc ctgc 34

<210> 54
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 54
gatggccgtg gctactcgag atcctcgttg tcgtag 36

<210> 55
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 55
ggcaattgag gaagaagctg ggca 24

<210> 56
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic

Oligonucleotide

<400> 56
ccatcacagc tagctgcagc 20

<210> 57
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 57
ccagaacctg aagcgtggcc acagcaacaa acacaaca 38

<210> 58
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 58
ggccatggaa gacgccaaaa ac 22

<210> 59
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 59
ggggcccggt acccggggat cc 22

<210> 60
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 60
gcaaagacat tgaatcaatt gtccttcac ctaaagca 38

<210> 61
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic

Oligonucleotide

<400> 61
agagggcgag gacgagatat cccacccacc aagcgga 37

<210> 62
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 62
gaatctcgat caagcgatat caaaatggcc gtaagaa 37

<210> 63
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 63
tgtgtgagga ggtacgatat cagttctttt gacttc 36

<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 64
aacaattgga ggagcggagg cgga 24

<210> 65
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 65
aaccatggaa tcctcgttgt cgtagtc 27

<210> 66
<211> 1073
<212> DNA
<213> Oryza sativa

<220>
<221> unsure

<222> (525)

<223> n=a,c,g or t

<400> 66

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cttttttttg ggggtgggat tcgcctggtc aagtgccatc gtcggatcat ggcggcggag 180
gcggcagcgg cgctggaggg gagcgagccc gtggacctgg ccaagcacc ctccggcatc 240
atccccacgc tccaaaacat cgtatcgacg gtcaatttgg attgcaaatt agacctcaaa 300
gctatagctt tgcaagctcg caatgcagaa tataatccaa agcgttttgc tgcggttattc 360
atgagaataa gagaacccaa aactacagct ctgatatattg catcggttaa aatggtctgt 420
actggggcaa agagtgaaca acaatccaag cttgcagcaa gaaagtacgc tcgtattatc 480
cagaagcttg gctttcctgc taaattcaag gatttcaaga ttcanaacat tgttggctct 540
tgtgatgtta aatttccaat caggctggag ggacttgcat attctcatgg tgccttctca 600
agtatgagc cagaactctt tcctggtctg atatatcgga tgaagcaacc aaagattgtt 660
cttctgattt ttgtttcagg caagattgtt ttgaccggag caaaggtgag ggatgagacg 720
tataccgcct ttgagaacat ataccctgtg ctaacggagt tcagaaaagt ccagcagtga 780
aaacttatgg aatacacaag tacaagcttc cttgagattt tgctgcctag tgactgctaa 840
tcttaactgt acatatggtc tggaggagcg tatagcatct tgtaatttat gtgagcccct 900
cgatgcacga gtgttgtaga cttgtttag taggcttgta gcttggtgta ctgagagact 960
tgagtatcgc gttcagtcga acgaggtgga gacgtggagt tatcgtactt tagcccgtgc 1020
tgattttttt cccttcacaa atagatctgt agcgaacat tttattacag aaa 1073
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<210> 67

<211> 203

<212> PRT

<213> *Oryza sativa*

<220>

<221> UNSURE

<222> (119)

<223> Xaa=ANY AMINO ACID

<400> 67

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Leu Ala Lys His Pro Ser Gly Ile Ile Pro Thr Leu Gln Asn Ile Val
      20                      25                      30

Ser Thr Val Asn Leu Asp Cys Lys Leu Asp Leu Lys Ala Ile Ala Leu
      35                      40                      45

Gln Ala Arg Asn Ala Glu Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile
      50                      55                      60

Met Arg Ile Arg Glu Pro Lys Thr Thr Ala Leu Ile Phe Ala Ser Gly
      65                      70                      75                      80

Lys Met Val Cys Thr Gly Ala Lys Ser Glu Gln Gln Ser Lys Leu Ala
      85                      90                      95

Ala Arg Lys Tyr Ala Arg Ile Ile Gln Lys Leu Gly Phe Pro Ala Lys
      100                      105                      110

Phe Lys Asp Phe Lys Ile Xaa Asn Ile Val Gly Ser Cys Asp Val Lys
      115                      120                      125

Phe Pro Ile Arg Leu Glu Gly Leu Ala Tyr Ser His Gly Ala Phe Ser
      130                      135                      140
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Ser Tyr Glu Pro Glu Leu Phe Pro Gly Leu Ile Tyr Arg Met Lys Gln
145 150 155 160

Pro Lys Ile Val Leu Leu Ile Phe Val Ser Gly Lys Ile Val Leu Thr
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Gly Ala Lys Val Arg Asp Glu Thr Tyr Thr Ala Phe Glu Asn Ile Tyr
180 185 190

Pro Val Leu Thr Glu Phe Arg Lys Val Gln Gln
195 200

<210> 68
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 68
gccatcgtcg gatccatggc ggcggaggcg 30

<210> 69
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 69
ccataagttt tcactcgagc tgctggactt t 31